

Method for Producing a Polynucleotide Library

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims, under 35 U.S.C. 119, the benefit of Danish application no. PA 2000 01828, filed December 6, 2000, and PA 2000 01853 filed on December 11, 2000 and U.S. provisional application no. 60/256,018, filed December 15, 2000, the contents of which are fully incorporated herein by reference.

Field of Invention

A method for making a plurality of new recombined polynucleotides by using a mismatch repair protein(s) or enzyme(s) to recombine at least two variants of the same polynucleotide or at least two homologous polynucleotides by Recombinatorial Chain Reaction, RCR.

Background of the Invention

The mismatch repair system is a system within cells which recognizes strand-strand nucleotide mismatches in newly synthesized duplex DNA sequences by comparing the new polynucleotide strand with the "old" polynucleotide strand originating from the parental duplex DNA, especially following DNA replication. The mismatch repair system of e.g. *Escherichia coli* corrects the strand-strand nucleotide mismatches by using the methylated "old" strand of the new duplex DNA as a template.

Independently of the molecular mechanism, the mismatch repair system normally limits the genetic diversity within a cell; where diversity in this context means the number of different DNA sequences. For example, a heteroduplex polynucleotide which comprises a single mismatch represents a diversity of two, since after one round of replication, the heteroduplex with the mismatch will have become two different double-stranded homoduplexes (with a one base pair difference between the two, originating from the mismatch in the parental heteroduplex).

However if the mismatch repair system corrects the mismatch in a heteroduplex before replication, the result will be two identical homoduplex DNA sequences, consequently the genetic diversity would be reduced to only one.

Several strategies and methods for generating genetic diversity are known in the art, such as classical random mutagenesis, site-directed mutagenesis, gene-shuffling etc. However,

there is still a need for new methods and ways to produce diverse polynucleotide sequences that may encode polypeptides with new properties or may have new properties themselves.

The state of the art shuffling methods are very efficient in shuffling polynucleotides comprising mutations that are located far apart in the polynucleotide sequences. However, 5 shuffling or recombining mutations that are positioned in relative close vicinity within a polynucleotide molecule has remained a challenge so far.

The present invention provides a method of utilizing a mismatch repair protein(s) or enzyme(s) to increase the genetic diversity in a polynucleotide population from a starting material of at least two homologous polynucleotides, to obtain a plurality of new recombined 10 homologous polynucleotides. The method of the invention even allows for the shuffling or recombining of homologous polynucleotide sequences, where the sequence variation(s) between the at least two parental starting sequences are closely located in the polynucleotide sequence.

The method of the invention utilizes a mismatch repair protein(s) as known in the art 15 (Biswas and Hsieh, 1996, Identification and Characterization of a Thermostable MutS Homologue from *Thermus aquaticus*, J Biol Chem 271(9):5040-5048) and (Sugahara et al., 2000, Crystal structure of a repair enzyme of oxidatively damaged DNA, MutM (Fpg), from an extreme thermophile, *Thermus thermophilus* HB8, J EMBO 19(15):3857-3869).

20 **Summary of the Invention:**

The problem to be solved by the present invention is how to generate diverse polynucleotide libraries that comprise new recombined polynucleotides, from a starting material comprising homologous template polynucleotides. A cell population comprising such a library may then be used to screen for a particular property/activity of interest encoded by a 25 polynucleotide which can be selected on this basis. Also polynucleotide sequences with particular changed or improved properties might be selected, such as promoters, terminators and other regulatory elements.

The present inventor provides a method for increasing the genetic diversity from a starting material of at least two homologous double-stranded polynucleotides or at least two 30 variants of the same double-stranded polynucleotides such as two different DNA sequences encoding homologous polypeptides e.g. enzymes or pharmaceutically active peptides.

As mentioned above, the present invention even allows shuffling or recombining of homologous polynucleotide sequences, where the sequence variation(s) between the at least two parental starting sequences are closely located in the polynucleotide sequence e.g. the two

starting sequences may comprise variations that are only one or a few nucleotides away from each other.

Optionally the steps (b) through (d) of the method of the present invention may be repeated for one or more cycles; wherein the new duplexes of step (d) serve as new template polynucleotides in step (b) in each subsequent cycle. Increasing the number of repeats or cycles will result in an increase in the number of new recombined polynucleotides, as new permutations of mismatches will be generated in the annealing step of each cycle.

Accordingly, in a first aspect the present invention relates to a method for forming a plurality of recombined homologous double-stranded polynucleotides from at least two homologous double-stranded template polynucleotides, said method comprising the steps of:

- a) providing a solution comprising at least two non-methylated homologous double-stranded template polynucleotides and one or more mismatch repair protein(s);
- b) denaturing the template polynucleotides into single-stranded polynucleotides;
- c) annealing the different single-stranded polynucleotides, wherein heteroduplexes are formed;
- d) allowing the mismatch repair protein(s) to repair nucleotide mismatches in the heteroduplexes, wherein recombined new duplexes are formed; and
- e) optionally, repeating steps b) through d) for one or more cycles; wherein the new duplexes of step d) serve as new template polynucleotides in step b) in each subsequent cycle.

In a second aspect the present invention relates to a plurality of recombined nucleotides generated by a method as defined in the first aspect.

A library of recombined polynucleotides generated by the method of the invention may be screened for a particular activity or property of interest, and a polynucleotide may be selected based on the results of such a screening.

Accordingly, in a third aspect the invention relates to a recombined polynucleotide generated by a method as defined in the first aspect.

Also, in a fourth aspect the invention relates to the use of a plurality of recombined polynucleotides of the second aspect generated by a method as defined in the first aspect, in a screening assay for an activity or property of interest.

In a final aspect the invention relates to the use of a recombined polynucleotide of the third aspect generated by a method as defined in the first aspect, for expression or production of a polypeptide of interest.

Definitions

Following section provides definitions of technical features in above mentioned aspects of the invention.

The term "a gene" denotes herein a gene (a polynucleotide) which is capable of being expressed into a polypeptide within a living cell or by an appropriate expression system. Accordingly, said gene is defined as an open reading frame starting from a start codon (normally "ATG", "GTG", or "TTG") and ending at a stop codon (normally "TAA", TAG" or "TGA"). In order to express said gene there must be elements, as known in the art, in connection with the gene, necessary for expression of the gene within the cell. Such standard elements may include a promoter, a ribosomal binding site, a termination sequence, and maybe others elements as known in the art.

The term "substantially pure polynucleotide" as used herein refers to a polynucleotide preparation, wherein the polynucleotide has been removed from its natural genetic milieu, and is thus free of other extraneous or unwanted coding sequences and is in a form suitable for use within genetically engineered protein production systems.

Thus, a substantially pure polynucleotide contains at the most 10% by weight of other polynucleotide material with which it is natively associated (lower percentages of other polynucleotide material are preferred, e.g. at the most 8% by weight, at the most 6% by weight, at the most 5% by weight, at the most 4% at the most 3% by weight, at the most 2% by weight, at the most 1% by weight, and at the most ½% by weight). A substantially pure polynucleotide may, however, include naturally occurring 5' and 3' untranslated regions, such as promoters and terminators.

It is preferred that the substantially pure polynucleotide is at least 92% pure, i.e. that the polynucleotide constitutes at least 92% by weight of the total polynucleotide material present in the preparation, and higher percentages are preferred such as at least 94% pure, at least 95% pure, at least 96% pure, at least 96% pure, at least 97% pure, at least 98% pure, at least 99%, and at the most 99.5% pure.

The polynucleotides disclosed herein are preferably in a substantially pure form. In particular, it is preferred that the polynucleotides disclosed herein are in "essentially pure form", i.e. that the polynucleotide preparation is essentially free of other polynucleotide material with which it is natively associated. Herein, the term "substantially pure polynucleotide" is synonymous with the terms "isolated polynucleotide" and "polynucleotide in isolated form".

The term "homologous" in the present context means that the two homologous polynucleotides or polypeptides have a "degree of identity" of at least 60%, more preferably at

least 70%, even more preferably at least 85%, still more preferably at least 90%, more preferably at least 95%, and most preferably at least 98%. Whether two polynucleotide or polypeptide sequences have a sufficiently high degree of identity to be homologous as defined herein, can suitably be investigated by aligning the two sequences using a computer program known in the art, such as "GAP" provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711)(Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-453). Using GAP with the following settings for DNA sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3.

A "heteroduplex" is used herein as having the meaning known in the art, which means that a heteroduplex is a double-stranded polynucleotide, such as a double-stranded DNA-molecule, wherein several base- or nucleotide-pairs are mismatched or, in other words, the two strands are not perfectly complementary.

The term "homoduplex" has the well-described meaning known in the art, a double-stranded polynucleotide wherein the two strands are perfectly complementary and no nucleotide-pair mismatches are found *i.e.* all adenosines pair with a thymidine (A's pair with T's) and all guanosines pair with a cytidine (G's pair with C's).

The term "duplex" as used herein is defined as a double-stranded polynucleotide which may be either a hetero- or a homoduplex polynucleotide as defined above.

The term "denaturing" is used herein as known in the art, for example a double-stranded polynucleotide comprised in a liquid solution may be denatured by heating the solution to at least the melting-point or melting-temperature of the double-stranded polynucleotide and keeping the solution at that temperature until the double-stranded polynucleotide has denatured, separated, or "melted" into two complementary single-stranded polynucleotides.

"Annealing" as used herein means that conditions such as temperature and salt-concentrations in a liquid solution are so that a single-stranded polynucleotide comprised in the solution will anneal preferentially to another single-stranded homologous polynucleotide comprised in the solution, in other words polynucleotides that are not homologous will not anneal to any significant extent.

"Nucleic acid construct" when used herein, the term nucleic acid construct means a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring source or which has been modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature. The term nucleic acid construct is synonymous with

the term "expression cassette" when the nucleic acid construct contains the control sequences required for expression of a coding sequence of the present invention.

"Control sequence" is defined herein to comprise all components that are necessary or advantageous for the expression of a polynucleotide of the present invention. Each control sequence may be native or foreign to the nucleotide sequence encoding the polypeptide. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the nucleotide sequence encoding a polypeptide.

"Operably linked" is defined herein as a configuration in which a control sequence is appropriately placed at a position relative to the coding sequence of the polynucleotide sequence such that the control sequence directs the expression of the polynucleotide.

"Coding sequence" is intended to cover a polynucleotide sequence, which directly specifies the amino acid sequence of its protein product. The boundaries of the coding sequence are generally determined by an open reading frame, which usually begins with the ATG start codon. The coding sequence typically include DNA, cDNA, and recombinant nucleotide sequences.

In the present context, the term "expression" includes any step involved in the production of a polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

In the present context, the term "expression vector" covers a polynucleotide molecule, linear or circular, that comprises a polynucleotide segment encoding a polypeptide of interest, and which is operably linked to additional segments that provide for the expression.

The term "host cell", as used herein, is defined below.

The term "mismatch repair system" shall herein be understood according to the art, as a system normally present within cells which recognises mismatches in duplex DNA sequences; see e.g. WO 97/37011, page 1, line 21-28. The mismatch repair system either corrects the mismatches by e.g. using the methylated "old" strand as template or alternatively the system may mediate degradation of the duplex DNA sequences which comprise the mismatches. Independently of the precise molecular mechanism, the end result will be that the "mismatch repair system" normally limits the "diversity" within the cell, represented by those duplex DNA sequences that comprise mismatches. The instant invention however utilizes the very base pair

mismatch-correcting property of the mismatch repair system to generate diversity instead of limiting it. When non-methylated double-stranded polynucleotides comprising mismatches are treated with a mismatch repair protein(s), the result will be unpredictable error-corrections in both strands, as there is no discernable template strand for the protein(s) to use for proofreading. This means that various new nucleotides may be introduced in either polynucleotide strand of the heteroduplex in the process of forming a new recombined duplex with a reduced number of mismatches or no mismatches at all. The mismatch repair system preferably comprises a MutS homologue, preferably MutS YT1 of *Thermus aquaticus*, or comprises a MutL homologue, a MSH2 homologue, a MSH6 homologue, a MutM homologue, a MutY homologue, a MutT homologue, a MutH homologue, a HexA homologue, a HexB homologue, or a GTBP/p160 homologue (Biswas and Hsieh, 1996, vide supra).

The term "solution" denotes any liquid solution, such as an aqueous solution, comprising the at least two homologous double-stranded template polynucleotides and one or more mismatch repair protein(s).

The term "DNA library", "polynucleotide library", or "plurality of polynucleotides" denotes herein a library of at least two different DNA sequences. For many practical purposes the library is much bigger. Accordingly, the DNA library preferably comprises at least 1000 different DNA sequences, more preferably at least 10000 different DNA sequences, and even more preferably at least 100000 different DNA sequences.

In the present context, the term "allelic variant" denotes any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequences. An allelic variant of a polypeptide is a polypeptide encoded by an allelic variant of a gene.

The term "thermostable" protein(s) in the present context means that the protein(s) remains essentially functional after having been exposed to the relatively high temperatures needed to denature the double-stranded polynucleotides in step (b) of the method of the invention. Specifically the thermostable protein(s) retains from at least 60% to 80% of its activity at its optimum temperature after one denaturing step; wherein the activity may be determined by the ATP-hydrolysis (ATPase) assay described in (Biswas and Hsieh, 1996, vide supra) which is incorporated herein by reference.

Detailed Description of the Invention

A method for forming a plurality of recombined homologous double-stranded polynucleotides from at least two homologous double-stranded template polynucleotides according to the first aspect of the invention.

5 The techniques used to isolate or clone a polynucleotide sequence are known in the art and include isolation from genomic DNA, preparation from cDNA, or a combination thereof. The cloning of the polynucleotide sequences of the present invention from such genomic DNA can be effected, e.g., by using the well known polymerase chain reaction (PCR), expression cloning, or antibody screening of expression libraries to detect cloned DNA fragments with
10 shared structural features. See, e.g., Innis *et al.*, 1990, *PCR: A Guide to Methods and Application*, Academic Press, New York. Other amplification procedures such as ligase chain reaction (LCR), ligated activated transcription (LAT) and nucleotide sequence-based amplification (NASBA) may be used. The nucleotide sequence may be cloned from a bacterial or fungal strain or another or related organism and thus, for example, may be an allelic or
15 species variant of the polypeptide encoding region of the nucleotide sequence.

The polynucleotide sequence may be obtained by standard cloning procedures used in genetic engineering to relocate the polynucleotide sequence from its natural location to a different site where it will be reproduced. The cloning procedures may involve excision and isolation of a desired polynucleotide fragment comprising the polynucleotide sequence of
20 interest, insertion of the fragment into a vector molecule, and incorporation of the resulting recombinant vector into a host cell where multiple copies or clones of the polynucleotide sequence will be replicated. The polynucleotide sequence may be of genomic, cDNA, RNA, semi synthetic, synthetic origin, or any combinations thereof.

Accordingly a preferred embodiment of the invention relates to a method of the first
25 aspect, wherein the at least two homologous double-stranded template polynucleotides are obtained by PCR amplification.

There is a substantial commercial interest in polypeptides such as pharmaceutically active peptides or industrial enzymes, and there is much research focused on changing or improving the properties or activities of such polypeptides. Terms like "protein engineering" or
30 "gene shuffling" are frequently encountered in the art. The present invention provides a new way of recombining polynucleotide sequences without having to fragment the template polynucleotides or synthesize a large number of overlapping primers to be used in a PCR reaction etc.

The method of the invention allows specific non-determined sequence variations to be recombined between homologous annealed polynucleotides via the action of a mismatch repair protein(s) which exchanges nucleotides in the polynucleotide sequences where there is a mismatch between the homologous strands, to provide new recombined polynucleotide strands, thus increasing the genetic diversity. A requirement for the method to function is that at least two homologous polynucleotide strands are able to anneal under the conditions given and this ability will largely depend on the degree of identity between the two polynucleotide strands which should preferably be at least 60%, more preferably at least 70%, even more preferably at least 85%, still more preferably at least 90%, more preferably at least 95%, and most preferably at least 98%.

It is well known in the art that polynucleotide sequences encoding certain polypeptides with similar properties or activities, such as enzymes, are often highly homologous. The homologous polynucleotides and polypeptides may be species variants or allelic variants descending from a common ancestral sequence which have evolved separately to the present day.

A template polynucleotide may encode an enzymatic polypeptide e.g. an aminopeptidase, an amylase, a carbohydrase, a carboxypeptidase, a catalase, a cellulase, a chitinase, a cutinase, a cyclodextrin glycosyltransferase, a deoxyribonuclease, an esterase, an alpha-galactosidase, a beta-galactosidase, a glucoamylase, an alpha-glucosidase, a beta-glucosidase, a haloperoxidase, an invertase, a laccase, a lipase, a mannosidase, an oxidase, a pectinolytic enzyme, a peroxidase, a phytase, a polyphenoloxidase, a proteolytic enzyme, a ribonuclease, or a xylanase.

Consequently, a preferred embodiment of the invention relates to the method of the first aspect, wherein the at least two homologous double-stranded template polynucleotides encode homologous polypeptides, preferably having a degree of identity of at least 60%, more preferably at least 70%, even more preferably at least 85%, still more preferably at least 90%, more preferably at least 95%, and most preferably at least 98%.

Another preferred embodiment of the invention relates to a method of the first aspect, wherein the at least two homologous double-stranded template polynucleotides encode homologous enzymes, preferably amylases, proteases, cellulases, lipases, xylanases, or phospholipases.

The homologous template polynucleotides may be comprised in a population of host cells which do not methylate polynucleotides or the gene encoding the mismatch repair protein(s) may be comprised in the same population of cells or in another cell population so that

the cells produce the repair protein(s). The cells may secrete the repair protein(s) or the cells may produce the repair protein(s) intracellularly; in the latter case it may be an advantage to lyse the cells prior to step (b) of the method of the invention.

Accordingly a preferred embodiment relates to a method of the first aspect, wherein
5 the solution comprises a population of cells or a lysate of a population of cells.

Further, a preferred embodiment relates to a method of the first aspect, wherein the population of cells or the lysate of a population of cells comprises the at least two homologous double-stranded template polynucleotides.

Still another preferred embodiment relates to a method of the first aspect, wherein the
10 population of cells or the lysate of a population of cells comprises the mismatch repair protein(s).

Yet another preferred embodiment relates to a method of the first aspect, wherein the population of cells, or the population of cells giving rise to the lysate, do not methylate newly synthesized polynucleotides.

As mentioned previously, the denaturing and annealing steps in the method of the
15 invention can be achieved by raising and subsequently lowering the temperature of the solution, however that would require the mismatch repair protein(s) to remain essentially functional after having been exposed to the relatively high temperatures needed to denature the double-stranded polynucleotides. It may be advantageous to use a thermostable mismatch repair
20 protein(s).

Accordingly a preferred embodiment relates to a method of the first aspect, wherein the mismatch repair protein(s) is (are) thermostable, preferably the thermostable mismatch repair protein(s) comprises a MutS homologue, preferably MutS YT1 of *Thermus aquaticus*, and more preferably the thermostable mismatch repair protein(s) comprises a MutL homologue,
25 a MSH2 homologue, a MSH6 homologue, a MutM homologue, a MutY homologue, a MutT homologue, a MutH homologue, a HexA homologue, a HexB homologue, or a GTBP/p160 homolog.

As mentioned previously the denaturing step in the method of the invention may be achieved by increasing the temperature of the solution.

Accordingly a preferred embodiment relates to a method of the first aspect, wherein
30 the denaturing is achieved by increasing the temperature of the solution, preferably to at least 90°C, more preferably to at least 91°C, more preferably to at least 92°C, even more preferably to at least 93°C, still more preferably to at least 94°C, more preferably to at least 95°C, and most preferably to at least 96°C.

As also mentioned above, the annealing step in the method of the invention may be performed by lowering the temperature of the solution, preferably by lowering the temperature at least to a temperature where the complementary homologous single-stranded polynucleotides preferentially anneal to each other and where the mismatch repair protein(s) functions.

Accordingly a preferred embodiment relates to a method of the first aspect, wherein the annealing is achieved by lowering the temperature of the solution, preferably at least to a temperature at which the mismatch repair protein(s) functions, more preferably at least to between 45°C and 85°C, more preferably at least to between 50°C and 80°C, more preferably at least to between 55°C and 75°C, and most preferably at least to between 60°C and 70°C.

We previously mentioned that the steps (b) through (d) of the method of the present invention may optionally be repeated for one or more cycles; wherein the new duplexes of step (d) serve as new template polynucleotides in step (b) in each subsequent cycle. Increasing the number of repeats or cycles will result in an increase in the number of new recombined polynucleotides, as new permutations of mismatches will be generated in the annealing step of each cycle.

Consequently a preferred embodiment relates to a method of the first aspect, wherein steps b) through d) are repeated for between 1 and 10 cycles; wherein the new duplexes of step d) serve as new template polynucleotides in step b) in each subsequent cycle.

Another preferred embodiment relates to a method of the first aspect, wherein steps b) through d) are repeated for at least 10 cycles; wherein the new duplexes of step d) serve as new template polynucleotides in step b) in each subsequent cycle.

A polynucleotide library obtained by the method of the invention may be expressed and assayed in a screen for a particular property/activity of interest encoded by a polynucleotide which can be selected on this basis. Also polynucleotide sequences with particular changed or improved properties might be selected, such as promoters, terminators and other regulatory elements.

The present invention also relates to nucleic acid constructs comprising a nucleotide sequence of the present invention operably linked to one or more control sequences that direct the expression of the coding sequence in a suitable host cell under conditions compatible with the control sequences.

A polynucleotide sequence of the present invention may be manipulated in a variety of ways to provide e.g. for expression of an encoded polypeptide. Manipulation of the nucleotide sequence prior to its insertion into a vector may be desirable or necessary depending on the

expression vector. The techniques for modifying nucleotide sequences utilizing recombinant DNA methods are well known in the art.

The control sequence may be an appropriate promoter sequence, a nucleotide sequence which is recognized by a host cell for expression of the nucleotide sequence. The promoter sequence contains transcriptional control sequences, which mediate the expression of the polypeptide. The promoter may be any nucleotide sequence which shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

Examples of suitable promoters for directing the transcription of the nucleic acid constructs of the present invention, especially in a bacterial host cell, are the promoters obtained from the *E. coli lac* operon, *Streptomyces coelicolor* agarase gene (*dagA*), *Bacillus subtilis* levansucrase gene (*sacB*), *Bacillus licheniformis* alpha-amylase gene (*amyL*), *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), *Bacillus amyloliquefaciens* alpha-amylase gene (*amyQ*), *Bacillus licheniformis* penicillinase gene (*penP*), *Bacillus subtilis* *xylA* and *xylB* genes, and prokaryotic beta-lactamase gene (Villa-Kamaroff *et al.*, 1978, *Proceedings of the National Academy of Sciences USA* 75: 3727-3731), as well as the *tac* promoter (DeBoer *et al.*, 1983, *Proceedings of the National Academy of Sciences USA* 80: 21-25). Further promoters are described in "Useful proteins from recombinant bacteria" in *Scientific American*, 1980, 242: 74-94; and in Sambrook *et al.*, 1989, *supra*.

Examples of suitable promoters for directing the transcription of the nucleic acid constructs of the present invention in a filamentous fungal host cell are promoters obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (*glaA*), *Rhizomucor miehei* lipase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate isomerase, *Aspergillus nidulans* acetamidase, and *Fusarium oxysporum* trypsin-like protease (WO 96/00787), as well as the NA2-tpi promoter (a hybrid of the promoters from the genes for *Aspergillus niger* neutral alpha-amylase and *Aspergillus oryzae* triose phosphate isomerase), and mutant, truncated, and hybrid promoters thereof.

In a yeast host, useful promoters are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* galactokinase (GAL1), *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP),

and *Saccharomyces cerevisiae* 3-phosphoglycerate kinase. Other useful promoters for yeast host cells are described by Romanos *et al.*, 1992, *Yeast* 8: 423-488.

The control sequence may also be a suitable transcription terminator sequence, a sequence recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3' terminus of the nucleotide sequence encoding the polypeptide. Any terminator which is functional in the host cell of choice may be used in the present invention.

Preferred terminators for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* alpha-glucosidase, and *Fusarium oxysporum* trypsin-like protease.

Preferred terminators for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase, *Saccharomyces cerevisiae* cytochrome C (CYC1), and *Saccharomyces cerevisiae* glyceraldehyde-3-phosphate dehydrogenase. Other useful terminators for yeast host cells are described by Romanos *et al.*, 1992, *supra*.

The control sequence may also be a suitable leader sequence, a nontranslated region of an mRNA which is important for translation by the host cell. The leader sequence is operably linked to the 5' terminus of the nucleotide sequence encoding the polypeptide. Any leader sequence that is functional in the host cell of choice may be used in the present invention.

Preferred leaders for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase and *Aspergillus nidulans* triose phosphate isomerase.

Suitable leaders for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* 3-phosphoglycerate kinase, *Saccharomyces cerevisiae* alpha-factor, and *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP).

The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3' terminus of the nucleotide sequence and which, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence which is functional in the host cell of choice may be used in the present invention.

Preferred polyadenylation sequences for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Fusarium oxysporum* trypsin-like protease, and *Aspergillus niger* alpha-glucosidase.

Useful polyadenylation sequences for yeast host cells are described by Guo and Sherman, 1995, *Molecular Cellular Biology* 15: 5983-5990.

The control sequence may also be a signal peptide coding region that codes for an amino acid sequence linked to the amino terminus of a polypeptide and directs the encoded polypeptide into the cell's secretory pathway. The 5' end of the coding sequence of the nucleotide sequence may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted polypeptide. Alternatively, the 5' end of the coding sequence may contain a signal peptide coding region which is foreign to the coding sequence. The foreign signal peptide coding region may be required where the coding sequence does not naturally contain a signal peptide coding region. Alternatively, the foreign signal peptide coding region may simply replace the natural signal peptide coding region in order to enhance secretion of the polypeptide. However, any signal peptide coding region which directs the expressed polypeptide into the secretory pathway of a host cell of choice may be used in the present invention.

Effective signal peptide coding regions for bacterial host cells are the signal peptide coding regions obtained from the genes for *Bacillus* NCIB 11837 maltogenic amylase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus licheniformis* subtilisin, *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* neutral proteases (*nprT*, *nprS*, *nprM*), and *Bacillus subtilis* *prsA*. Further signal peptides are described by Simonen and Palva, 1993, *Microbiological Reviews* 57: 109-137.

Effective signal peptide coding regions for filamentous fungal host cells are the signal peptide coding regions obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* neutral amylase, *Aspergillus niger* glucoamylase, *Rhizomucor miehei* aspartic proteinase, *Humicola insolens* cellulase, and *Humicola lanuginosa* lipase.

Useful signal peptides for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* alpha-factor and *Saccharomyces cerevisiae* invertase. Other useful signal peptide coding regions are described by Romanos *et al.*, 1992, *supra*.

The control sequence may also be a propeptide coding region that codes for an amino acid sequence positioned at the amino terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to a mature active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding region may be obtained from the genes for *Bacillus subtilis* alkaline protease (*aprE*), *Bacillus subtilis*

neutral protease (*nprT*), *Saccharomyces cerevisiae* alpha-factor, *Rhizomucor miehei* aspartic proteinase, and *Myceliophthora thermophila* laccase (WO 95/33836).

Where both signal peptide and propeptide regions are present at the amino terminus of a polypeptide, the propeptide region is positioned next to the amino terminus of a polypeptide and the signal peptide region is positioned next to the amino terminus of the propeptide region.

It may also be desirable to add regulatory sequences which allow the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those which cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory systems in prokaryotic systems include the *lac*, *tac*, and *trp* operator systems. In yeast, the ADH2 system or GAL1 system may be used. In filamentous fungi, the TAKA alpha-amylase promoter, *Aspergillus niger* glucoamylase promoter, and *Aspergillus oryzae* glucoamylase promoter may be used as regulatory sequences. Other examples of regulatory sequences are those which allow for gene amplification. In eukaryotic systems, these include the dihydrofolate reductase gene which is amplified in the presence of methotrexate, and the metallothionein genes which are amplified with heavy metals. In these cases, the nucleotide sequence encoding the polypeptide would be operably linked with the regulatory sequence.

Accordingly a preferred embodiment relates to a method of the first aspect, wherein additional steps are performed, said additional steps comprising:

- f) generating a gene library by cloning the plurality of recombined polynucleotides;
- g) expressing and screening the gene library for an activity or property of interest; and
- h) isolating or identifying the recombined polynucleotide which gives rise to the activity or property of interest.

The present invention also relates to recombinant expression vectors comprising the polynucleotides of the invention especially when those are comprised in a nucleic acid construct such as an expression vector. The various nucleotide and control sequences described above may be joined together to produce a recombinant expression vector which may include one or more convenient restriction sites to allow for insertion or substitution of the polynucleotide sequence at such sites.

Alternatively, a polynucleotide sequence of the present invention may be expressed by inserting the nucleotide sequence or a nucleic acid construct comprising the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

The recombinant expression vector may be any vector (e.g., a plasmid or virus) which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of the nucleotide sequence. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The
5 vectors may be linear or closed circular plasmids.

The vector may be an autonomously replicating vector, i.e., a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome.

10 The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host cell, or a transposon may be used.

15 The vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

20 Examples of bacterial selectable markers are the *dal* genes from *Bacillus subtilis* or *Bacillus licheniformis*, or markers which confer antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracycline resistance. Suitable markers for yeast host cells are ADE2, HIS3, LEU2, LYS2, MET3, TRP1, and URA3. Selectable markers for use in a filamentous fungal host cell include, but are not limited to, *amdS* (acetamidase), *argB* (ornithine carbamoyltransferase), *bar* (phosphinothricin acetyltransferase), *hygB* (hygromycin
25 phosphotransferase), *niaD* (nitrate reductase), *pyrG* (orotidine-5'-phosphate decarboxylase), *sC* (sulfate adenylyltransferase), *trpC* (anthranilate synthase), as well as equivalents thereof.

Preferred for use in an *Aspergillus* cell are the *amdS* and *pyrG* genes of *Aspergillus nidulans* or *Aspergillus oryzae* and the *bar* gene of *Streptomyces hygrosopicus*.

30 The vectors of the present invention preferably contain an element(s) that permits stable integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

For integration into the host cell genome, the vector may rely on the nucleotide sequence encoding the polypeptide or any other element of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination.

Alternatively, the vector may contain additional nucleotide sequences for directing integration by homologous recombination into the genome of the host cell. The additional nucleotide sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s).

5 To increase the likelihood of integration at a precise location, the integrational elements should preferably contain a sufficient number of nucleotides, such as 100 to 1,500 base pairs, preferably 400 to 1,500 base pairs, and most preferably 800 to 1,500 base pairs, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be any sequence that
10 is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding nucleotide sequences. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

For autonomous replication, the vector may further comprise an origin of replication
15 enabling the vector to replicate autonomously in the host cell in question. Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, and pACYC184 permitting replication in *E. coli*, and pUB110, pE194, pTA1060, and pAM β 1 permitting replication in *Bacillus*. Examples of origins of replication for use in a yeast host cell
20 are the 2 micron origin of replication, ARS1, ARS4, the combination of ARS1 and CEN3, and the combination of ARS4 and CEN6. An example of a filamentous fungal stabilizing element is the AMA1 sequence. The origin of replication may be one having a mutation which makes its functioning temperature-sensitive in the host cell (see, e.g., Ehrlich, 1978, *Proceedings of the National Academy of Sciences USA* 75: 1433).

More than one copy of a nucleotide sequence of the present invention may be inserted
25 into the host cell to increase production of the gene product. An increase in the copy number of the nucleotide sequence can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the nucleotide sequence where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the nucleotide sequence, can be selected for by cultivating the
30 cells in the presence of the appropriate selectable agent.

The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, e.g., Sambrook *et al.*, 1989, *supra*).

The present invention also relates to recombinant a host cell comprising the polynucleotide(s) or nucleic acid construct(s) of the invention, which are advantageously used in the screening assays described herein. A vector comprising a nucleotide sequence of the present invention is introduced into a host cell so that the vector is maintained as a chromosomal integrant or as a self-replicating extra-chromosomal vector as described earlier.

The host cell may be a unicellular microorganism, e.g., a prokaryote, or a non-unicellular microorganism, e.g., a eukaryote.

Useful unicellular cells are bacterial cells such as gram positive bacteria including, but not limited to, a *Bacillus* cell, e.g., *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis*; or a *Streptomyces* cell, e.g., *Streptomyces lividans* or *Streptomyces murinus*, or gram negative bacteria such as *E. coli* and *Pseudomonas* sp.

In a preferred embodiment, the bacterial host cell is a *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus stearothermophilus*, or *Bacillus subtilis* cell. In another preferred embodiment, the *Bacillus* cell is an alkalophilic *Bacillus*.

The introduction of a vector into a bacterial host cell may, for instance, be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, *Molecular General Genetics* 168: 111-115), using competent cells (see, e.g., Young and Spizizin, 1961, *Journal of Bacteriology* 81: 823-829, or Dubnau and Davidoff-Abelson, 1971, *Journal of Molecular Biology* 56: 209-221), electroporation (see, e.g., Shigekawa and Dower, 1988, *Biotechniques* 6: 742-751), or conjugation (see, e.g., Koehler and Thorne, 1987, *Journal of Bacteriology* 169: 5771-5278).

The host cell may be a eukaryote, such as a mammalian, insect, plant, or fungal cell.

In a preferred embodiment, the host cell is a fungal cell. "Fungi" as used herein includes the phyla Ascomycota, Basidiomycota, Chytridiomycota, and Zygomycota (as defined by Hawksworth *et al.*, In, *Ainsworth and Bisby's Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK) as well as the Oomycota (as cited in Hawksworth *et al.*, 1995, *supra*, page 171) and all mitosporic fungi (Hawksworth *et al.*, 1995, *supra*).

In a more preferred embodiment, the fungal host cell is a yeast cell. "Yeast" as used herein includes ascosporeogenous yeast (Endomycetales), basidiosporeogenous yeast, and yeast belonging to the Fungi Imperfecti (Blastomycetes). Since the classification of yeast may change in the future, for the purposes of this invention, yeast shall be defined as described in

Biology and Activities of Yeast (Skinner, F.A., Passmore, S.M., and Davenport, R.R., eds, Soc. App. Bacteriol. Symposium Series No. 9, 1980).

In an even more preferred embodiment, the yeast host cell is a *Candida*, *Hansenula*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomyces*, or *Yarrowia* cell.

5 In a most preferred embodiment, the yeast host cell is a *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis* or *Saccharomyces oviformis* cell. In another most preferred embodiment, the yeast host cell is a *Kluyveromyces lactis* cell. In another most preferred embodiment, the yeast host cell is a *Yarrowia lipolytica* cell.

10 In another more preferred embodiment, the fungal host cell is a filamentous fungal cell. "Filamentous fungi" include all filamentous forms of the subdivision Eumycota and Oomycota (as defined by Hawksworth *et al.*, 1995, *supra*). The filamentous fungi are characterized by a mycelial wall composed of chitin, cellulose, glucan, chitosan, mannan, and other complex polysaccharides. Vegetative growth is by hyphal elongation and carbon catabolism is obligately aerobic. In contrast, vegetative growth by yeasts such as *Saccharomyces cerevisiae* is by budding of a unicellular thallus and carbon catabolism may be fermentative.

In an even more preferred embodiment, the filamentous fungal host cell is a cell of a species of, but not limited to, *Acremonium*, *Aspergillus*, *Fusarium*, *Humicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolytocladium*, or *Trichoderma*.

20 In a most preferred embodiment, the filamentous fungal host cell is an *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger* or *Aspergillus oryzae* cell. In another most preferred embodiment, the filamentous fungal host cell is a *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*,
25 *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecioides*, or *Fusarium venenatum* cell. In an even most preferred embodiment, the filamentous fungal parent cell is a *Fusarium venenatum* (Nirenberg sp. nov.) cell. In another most preferred embodiment, the filamentous fungal host cell is a *Humicola insolens*, *Humicola lanuginosa*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*,
30 *Penicillium purpurogenum*, *Thielavia terrestris*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei*, or *Trichoderma viride* cell.

Fungal cells may be transformed by a process involving protoplast formation, transformation of the protoplasts, and regeneration of the cell wall in a manner known *per se*.



Suitable procedures for transformation of *Aspergillus* host cells are described in EP 238 023 and Yelton *et al.*, 1984, *Proceedings of the National Academy of Sciences USA* 81: 1470-1474. Suitable methods for transforming *Fusarium* species are described by Malardier *et al.*, 1989, *Gene* 78: 147-156 and WO 96/00787. Yeast may be transformed using the procedures
5 described by Becker and Guarente, *In* Abelson, J.N. and Simon, M.I., editors, *Guide to Yeast Genetics and Molecular Biology, Methods in Enzymology*, Volume 194, pp 182-187, Academic Press, Inc., New York; Ito *et al.*, 1983, *Journal of Bacteriology* 153: 163; and Hinnen *et al.*, 1978, *Proceedings of the National Academy of Sciences USA* 75: 1920.

A plurality of recombinant polynucleotides of the second aspect generated by the
10 method of first aspect may be screened for a particular activity or property of interest, and a recombinant polynucleotide of the third aspect generated by the method of the first aspect may be selected from the plurality of the second aspect based on the results of such a screening.

An essential element in this screening process is the use of a plurality of recombinant nucleotides of the second aspect generated by a method of the first aspect, in a screening
15 assay for an activity or property of interest.

Examples

Example 1

Construction of an expression plasmid

Plasmids pENI1298 and pENI1299 were described in WO 00/24883. The plasmid pENI1298 was further developed in order to decrease plasmid size (thus improve transformation), improve expression (by improving promoter), have expression in *E. coli* for improved library screening (by improving same promoter), ease cloning (by introducing unique restriction sites downstream of promoter), ease cloning (by using the Gateway cloning
20 technology)

Plasmid pENI1960 was made using the Gateway Vector™ conversion system (Lifetechnology® cat no. 11828-019) by cutting pENI1902 with BamHI, filling the DNA ends using Klenow fragment polymerase and nucleotides (thus making blunt ends) followed by ligation to reading frame A Gateway™ PCR fragment. The cloning in the correct orientation was
30 confirmed by sequencing.

Plasmid pENI1902 was made in order to have a promoter that works in both *E.coli* and *Aspergillus*. This was done by unique site elimination using the “Chameleon double stranded site-directed mutagenesis kit” as recommended by Stratagene®.

Plasmid pENI1861 was used as template and the following primers were used as selection primers (“5’P” indicates a 5’ phosphorylation of the primer):

177996 (SEQ ID NO:1): 5’P gaatgacttggttgacgcgtcaccagtcac

135640 (SEQ ID NO:2): 5’P cttattagtaggttggtacttcgag

135638 (SEQ ID NO:3): 5’P gtccccagagtagtgtcactatgtcgaggcagttaag

The 080399J19 primer (SEQ ID NO:4) was used as mutagenic primer to introduce a –35 and –10 promoter consensus sequence (from *E.coli*) in the *Aspergillus* expression promoter. Introduction of the mutations was verified by sequencing.

080399J19 (SEQ ID NO:4):

5’P gtatgtcccttgacaatgcgatgtatcacatgatataattactagcaaggggaagccg
tgcttgg

Plasmid pENI1861 was made in order to have the state of the art *Aspergillus* promoter in the expression plasmid, as well as a number of unique restriction sites for cloning. A PCR fragment (app. 620 bp) was made using pMT2188 (see Example 5) as template and the following primers:

051199J1 (SEQ ID NO:5):

5’ cctctagatctcgagctcggtcaccggtggcctccgcggccgctggatccccagttgtg

1298TAKA (SEQ ID NO:6):

5’ gcaagcgcgcgcaatacatggtgttttgatcat

The fragment was cut BssHII and Bgl II, and cloned into pENI1849 which was also cut with BssHII and Bgl II. The cloning was verified by sequencing.

Plasmid pENI1849 was made in order to truncate the pyrG gene to the essential sequences for pyrG expression, in order to decrease the size of the plasmid, thus improving transformation frequency. A PCR fragment (app. 1800 bp) was made using pENI1299 as
5 template and the following primers:

270999J8 (SEQ ID NO:7): 5' tctgtgaggcctatggatctcagaac

270999J9 (SEQ ID NO:8): 5' gatgctgcatgcacaactgcacctcag

10

The PCR-fragment was cut with the restriction enzymes Stul and SphI, and cloned into pENI1298, also cut with Stul and SphI; the cloning was verified by sequencing.

Example 2

Preparation of a cell extract comprising MutS mismatch repair enzymes from *Thermus aquaticus* ATCC25105.

The cell extract is made as described by O'Grady G.M., McCarthy T.V., Vaughan P.M. (1997) Biochemical Society Transactions vol 25 p. 319-322.

Example 3

Three primers are made based on the *Thermomyces lanuginosa* lipase gene (EMBL accession no.: AF054513), where each primer contains two in-frame stopcodons (shown below in bold typeface) and a silent mutation (shown below in underlined italic typeface). In order to have a functional lipase gene, recombination has to take place between all three primers during
25 the Recombinatorial Chain Reaction (RCR) method of the invention. After RCR the primers are subjected to a round of PCR and a cloning step.

The following reaction is mixed to a total of 25 microliter:

10 microliter of cell extract, 40 pmol of primer 251000j2, 40 pmol of primer 251000j3, 40 pmol of primer 251000j4 in buffer (20 mM Tris/HCl pH 7.5, 5 mM MgCl₂, 0.1 mM Dithiothreitol, 0.1
30 mM EDTA).

251000j2 (SEQ ID NO:9):

5' atcgggaatcttaacttcgact**ag**taagaaattaatgacatttgctcc

251000j3 (SEQ ID NO:10):

5' atcgggaatcttaacttcgactagaaataaat_taatgacatttgctcc

5 251000j4rev (SEQ ID NO:11):

5' ggagcaaagtgcattaat_tattacaagtcgaagttaagattcccgat

The reaction-mix is placed in a PCR machine (e.g. Perkin Elmer® 2400) and the following Recombinatorial Chain Reaction (RCR) cycle was run 94°C 5 min, 30 times (94°C, 30 sec., 45°C 1 min, 72°C, 3 min). After the RCR reaction, the mix is purified by being spun on BioRad® Columns (Micro Bio-spin P-6™; Biorad®).

Two PCR reactions as listed below are run at the following protocol: 94°C, 5 min; 30 cycles of (94°C, 30 sec; 50°C, 1 min; 72°C, 2 min); 72°C, 5min.

15 PCR1 (app. 420 bp):

Use pENI1298 as template, 20 pmol primer 19072000j1 and 1 microliter of the purified RCR extract in a total of 20 microliter, along with PWO™ DNA polymerase (Boehringer Mannheim™).

20 Primer 19072000J1 (SEQ ID NO:12):

5' ggggacaagtttgtacaaaaaagcaggcttctctgaacaataaacccac

PCR2 (app.600 bp):

25 Use pENI1298 as template, 20 pmol primer 16062000j2 and 1 microliter of the purified RCR extract in a total of 20 microliter, along with PWO™ DNA polymerase (Boehringer Mannheim™).

Primer 16062000j2 (SEQ ID NO:13):

5' ggggaccactttgtacaagaaagctgggtcctagatctcgagctcggtcac

30

The PCR fragments PCR1 and PCR2 are purified from a 1.5 % agarose using a Qiagen™ gel extraction kit. A third PCR (PCR3) is run using 1 micro l of each purified PCR fragment, 20 pmol primer 16062000j2, 20 pmol primer 19072000j1 in a total of 20 microliter,

along with PWO™ polymerase (Boehringer Mannheim™). The PCR fragment PCR3 is purified using BioRad™ Columns (Micro Bio-spin P-6™).

The BP cloning reaction is made by mixing the PCR3 fragment with BP reaction buffer, pDONR201 vector and BP clonase mix (as recommended by Lifetechnology®). Plasmid pENI1960 is cut with Scal (in order to cleave in the ccdB gene), and mixed with the BP reaction and LR clonase mix (as recommended by Lifetechnology®) and transformed into *E. coli* DH10b (Life-Technology™ cat. no.18290-015).

The transformation is plated onto A+B minimal plates (Clark and Maaloe (1967) J. Mol Biol. Vol 23 p. 99- 112) supplemented with 1% olive oil , ampicillin (100 microgram/ml) and 25 microgram/ml leucine. Only those *E.coli* transformants that have the plasmid and express a functional lipase will grow on these plates.

A DNA preparation is made from each transformant and sequenced to confirm the functionality of the lipase gene, as well as to identify the silent mutation originating from the primers, thus confirming the that the recombination event during the RCR has taken place as expected.

Example 4

Three primers are made based on the *Thermomyces lanuginosa* lipase gene. Each primer contains 2 in-frame stopcodons (shown below in bold typeface) and a silent mutation (shown below in underlined italic typeface). In order to have a functional lipase gene, recombination has to take place between all three primers during the Recombinatorial Chain Reaction (RCR) method of the invention. After RCR the primers are subjected to a round of PCR and a cloning step.

The following reaction is mixed in a total of 25 microliter:

10 microliter of cell extract, 40 pmol of primer 251000j2, 40 pmol of primer 251000j3, 40 pmol of primer 251000j4 in buffer (20 mM Tris/HCl pH 7.5, 5 mM MgCl2, 0.1 mM Dithiothreitol, 0.1 mM EDTA).

The reaction-mix is placed in a PCR machine (e.g. Perkin Elmer® 2400) and the following Recombinatorial Chain Reaction (RCR) cycle was run 94°C 5 min, 30 times (94°C, 30 sec., 45°C 1 min, 72°C, 3 min). After the RCR reaction, the mix is purified by being spun on BioRad® Columns (Micro Bio-spin P-6™; Biorad®).

Two PCR reactions as listed below are run at the following protocol: 94°C, 5 min; 30 cycles of (94°C, 30 sec; 50°C, 1 min; 72°C, 2 min); 72°C, 5min.

PCR 1 (app. 420 bp):

Use pENI1298 as template, 20 pmol primer 19671 and 1 microliter of the purified RCR extract in a total of 20 microliter, along with PWO™ DNA polymerase (Boehringer Mannheim™).

5

Primer 19671 (SEQ ID NO:14): 5' ctccttctctgaacaataaaccc

PCR 2 (app.600 bp):

Use pENI1298 as template, 20 pmol primer 991213J5 and 1 microliter of the purified RCR extract in a total of 20 microliter, along with PWO™ DNA polymerase (Boehringer Mannheim™).

10

Primer 991213J5 (SEQ ID NO:15):

5' cctctagatctcgagctcggtcaccggtggcctccgcggccgctgcgccaggtgtcagtc
accctc

15

The two PCR fragments PCR1 and PCR2 are purified from a 1.5 % agarose using a Qiagen® gel extraction kit. A third PCR (PCR3) is run using 1 microliter of each purified PCR fragment, PCR1 and PCR2, 100 pmol primer 19671, 100 pmol primer 991213J5 in a total of 100 microliter, along with PWO™ polymerase (Boehringer Mannheim™). After the reaction, the PCR3 fragment is purified from the mix by being spun on BioRad™ Columns (Micro Bio-spin P-6™).

20

The PCR fragment PCR3 and pENI 1902 are both cut BamHI and SacII and the cut fragments are purified from a 1 % agarose gel using a Qiagen™ gel extraction kit. The fragment and the pENI1902 vector are ligated and transformed into *E. coli* DH10b.

25

The transformation is plated onto A+B minimal plates (Clark and Maaloe (1967) J. Mol Biol. Vol 23 p. 99- 112) supplemented with 1 % olive oil , 100 microgram/ml ampicillin and 25 microgram/ml leucine. Only those *E.coli* transformants that have the plasmid and express a functional lipase will grow on these plates.

30

A DNA preparation is made from each transformant and sequenced to confirm the functionality of the lipase gene, as well as to identify the silent mutation originating from the primers, thus confirming the that the recombination event during the RCR has taken place as expected.

Example 5

Construction of the expression plasmid pMT2188

The *Aspergillus oryzae* expression plasmid pCaHj 483 (WO 98/00529) consists of an expression cassette based on the *Aspergillus niger* neutral amylase II promoter fused to the *Aspergillus nidulans* triose phosphate isomerase non translated leader sequence (Pna2/tpi) and the *A. niger* amyloglycosidase terminator (Tamg). Also present on the plasmid is the *Aspergillus* selective marker *amdS* from *A. nidulans* enabling growth on acetamide as sole nitrogen source. These elements are cloned into the *E. coli* vector pUC19 (New England Biolabs). The ampicillin resistance marker enabling selection in *E. coli* of this plasmid was replaced with the URA3 marker of *Saccharomyces cerevisiae* that can complement a *pyrF* mutation in *E. coli*, the replacement was done in the following way:

The pUC19 origin of replication was PCR amplified from pCaHj483 with the primers:

142779 (SEQ ID NO:16): 5' ttgaattgaaaatagattgattttaaacttc

142780 (SEQ ID NO:17): 5' ttgcatgcatgtaatatggtcatagc

Primer 142780 introduces a *BbuI* site in the PCR fragment. The Expand PCR system (Roche Molecular Biochemicals, Basel, Switzerland) was used for the amplification following the manufacturers instructions for this and the subsequent PCR amplifications.

The URA3 gene was amplified from the general *S. cerevisiae* cloning vector pYES2 (Invitrogen corporation, Carlsbad, Ca, USA) using the primers:

140288 (SEQ ID NO:18): 5' ttgaattcatgggtaataactgatat

142778 (SEQ ID NO:19): 5' aaatcaatctatatttcaattcaattcatcatt

Primer 140288 introduces an *EcoRI* site in the PCR fragment. The two PCR fragments were fused by mixing them and amplifying using the primers 142780 and 140288 in the splicing by overlap method (Horton et al (1989) Gene, 77, 61-68).

The resulting fragment was digested with *EcoRI* and *BbuI* and ligated to the largest fragment of pCaHj 483 digested with the same enzymes. The ligation mixture was used to transform the *pyrF* *E.coli* strain DB6507 (ATCC 35673) made competent by the method of Mandel and Higa (Mandel, M. and A. Higa (1970) J. Mol. Biol. 45, 154). Transformants were selected on solid M9 medium (Sambrook et. al (1989) Molecular cloning, a laboratory manual,

2. edition, Cold Spring Harbor Laboratory Press) supplemented with 1 g/l casaminoacids, 500 µg/l thiamine and 10 mg/l kanamycin.

A plasmid from a selected transformant was termed pCaHj 527. ThePna2/tpi promoter present on pCaHj527 was subjected to site directed mutagenesis by a simple PCR approach.

5 Nucleotide 134 – 144 was altered from GTACTAAAACC to CCGTTAAATTT using the mutagenic primer 141223.

141223 (SEQ ID NO:20):

5' ggatgctgttgactccggaaatttaacggtttggtcttgcacccc

10

Nucleotide 423 – 436 was altered from ATGCAATTTAACT to CGGCAATTTAACGG using the mutagenic primer 141222:

141222 (SEQ ID NO:21):

15 5' ggtattgtcctgcagacggcaatttaacggcttctgcgaatcgc

The resulting plasmid was termed pMT2188.

Example 6

20 Three primers were made based on the *Thermomyces lanuginosa* lipase gene (EMBL accession no.: AF054513), where each primer contained two in-frame stop codons (shown below in bold typeface) and a silent mutation (shown below in underlined italic typeface). The following reactions were mixed to a total of 25 microliter: Either 0.1 microliter, 1 microliter or 10 microliter of cell extract (re-suspended in gel-filtration buffer after (NH₄)₂SO₄ precipitation), 40 pmol of primer 251000j2, 40 pmol of primer 251000j3, 40 pmol of primer 251000j4 in buffer (20 mM Tris/HCl pH 7.5, 5 mM MgCl₂, 0.1 mM Dithiothreitol, 0.1 mM EDTA).

Primer 251000j2 (SEQ ID NO:9); primer 251000j3 (SEQ ID NO:10); and primer 251000j4 (SEQ ID NO:22):

30 5' atcgggaatcttaacttcgacttgtaataaataatgacatttgctcc

The reaction-mixes were placed in a PCR machine (e.g. Perkin Elmer® 2400) and the following Recombinatorial Chain Reaction (RCR) cycle was run 94°C 1 min, 30 times (94°C, 30 sec., 45°C 1 min, 72°C, 3 min).

Two PCR reactions as listed below were run at the following protocol: 94°C, 5 min; 30 cycles of (94°C, 30 sec; 50°C, 1 min; 72°C, 2 min); 72°C, 5min.

PCR1 (app. 420 bp):

- 5 Using pENI1298 as template, 20 pmol primer 19671 and primer 251000J5 in a total of 20 microliter, along with PWO™ DNA polymerase (Boehringer Mannheim™) including buffer and dNTP.

Primer 251000J5 (SEQ ID NO:23): 5' gtcgaagttaagattcccgat

10

Primer 19671 (SEQ ID NO:24): 5' ctcccttctctgaacaataaaccc

PCR2 (app.600 bp):

- 15 Using pENI1298 as template, 20 pmol primer 115120 and 1 microliter of the RCR extract (either originating from 0.1 microliter, 1 microliter or 10 microliter of cell extract) in a total of 20 microliter, along with PWO™ DNA polymerase (Boehringer Mannheim™) including buffer and dNTP.

Primer 115120 (SEQ ID NO:25): 5' gctttgtgcagggtaaatc

20

The PCR fragments PCR1 and PCR2 were purified from a 1.5 % agarose using a Qiagen™ gel extraction kit. A third PCR (PCR3) was run using 1 microliter of each purified PCR fragment, 20 pmol primer 19671, 20 pmol primer 991213J5 in a total of 20 microliter, along with PWO™ polymerase (Boehringer Mannheim™) including buffer and dNTP. The PCR fragment PCR3
25 was purified using BioRad™ Columns (Micro Bio-spin P-6™).

Primer 991213J5 (SEQ ID NO:26):

5' cctctagatctcgagctcggtcaccggtggcctccgcggccgctgcgccaggtgtcag
tcaccctc

30

The PCR fragment PCR3 and a pENI 1902-derivative were both cut BamHI and SacII and the cut fragments were purified from a 1 % agarose gel using a Qiagen™ gel extraction kit. The fragment and the pENI1902-derived vector were ligated and transformed into *E. coli* DH10b.

A DNA preparation was made from 6 transformant and sequenced. Recombination had taken place in at least one case.

Example 7

Three primers were made based on the *Thermomyces lanuginosa* lipase gene (EMBL accession no.: AF054513), where each primer contained two in-frame stop codons (shown below in bold typeface) and a silent mutation (shown below in underlined italic typeface).

The following reactions are mixed to a total of 25 microliter: Either 0.1 microliter, 1 microliter or 10 microliter of cell extract (re-suspended in gel-filtration buffer after (NH₄)₂SO₄ precipitation), 40 pmol of primer 251000j2, 40 pmol of primer 251000j3, 40 pmol of primer 070801J1 in buffer (20 mM Tris/HCl pH 7.5, 5 mM MgCl₂, 0.1 mM EDTA, 1 mM ATP, 10 % glycerol).

Primer 251000j2 (SEQ ID NO:9); Primer 251000j3 (SEQ ID NO:10); and Primer 070801J1 (SEQ ID NO:27): 5' ggagcaaatgtcattaatttattacaagtcgaagttaagattcccgat

The reaction-mix is placed in a PCR machine (e.g. Perkin Elmer® 2400) and the following Recombinatorial Chain Reaction (RCR) cycle was run 94°C 5 min, 30 times (94°C, 30 sec., 45°C 1 min, 72°C, 3 min).

Two PCR reactions as listed below are run at the following protocol: 94°C, 1 min; 30 cycles of (94°C, 30 sec; 50°C, 1 min; 72°C, 2 min); 72°C, 5min.

PCR 1 (app. 420 bp):

Use pENI1298 as template, 20 pmol primer 19671 (SEQ ID NO:14) and 1 microliter of the purified RCR extract (either originating from 0.1 microliter, 1 microliter or 10 microliter of cell

extract) in a total of 20 microliter, along with PWO™ DNA polymerase (Boehringer Mannheim™).

PCR 2 (app.600 bp):

- 5 Use pENI1298 as template, 20 pmol primer 991213J5 (SEQ ID NO:15) and 1 microliter of the purified RCR extract (either originating from 0.1 microliter, 1 microliter or 10 microliter of cell extract) in a total of 20 microliter, along with PWO™ DNA polymerase (Boehringer Mannheim™).

10 The two PCR fragments from PCR1 and PCR2 are purified from a 1.5 % agarose using a Qiagen® gel extraction kit. A third PCR (PCR3) is run using 1 microliter of each purified PCR fragment, PCR1 and PCR2, 100 pmol primer 19671, 100 pmol primer 991213J5 in a total of 100 microliter, along with PWO™ polymerase (Boehringer Mannheim™). After the reaction, the PCR3 fragment is purified from the mix by being spun on BioRad™ Columns (Micro Bio-spin P-6™).

15 The PCR fragment PCR3 and pENI1861 are both cut BamHI and SacII and the cut fragments are purified from a 1 % agarose gel using a Qiagen™ gel extraction kit. The fragment and the pENI1861 vector are ligated and transformed into *E. coli* DH10b.

20 The transformation are plated onto both LB-plates containing 100 microgram/ml ampicillin and onto A+B minimal plates (Clark and Maaloe (1967) J. Mol Biol. Vol 23 p. 99- 112) supplemented with 1 % olive oil , 100 microgram/ml ampicillin and 25 microgram/ml leucine. Only those *E.coli* transformants that have the plasmid and express a functional lipase will grow on A+B minimal plates (Clark and Maaloe (1967) J. Mol Biol. Vol 23 p. 99- 112) supplemented with 1 % olive oil, 100 microgram/ml ampicillin and 25 microgram/ml leucin.

A DNA preparation is made from each transformant, and sequenced to confirm the functionality of the lipase gene, as well as to identify the silent mutation originating from the primers, thus confirming the that the recombination event during the RCR has taken place as expected

5 A DNA preparation is made from each transformant growing on the LB-plates containing 100 microgram/ml ampicillin, and sequenced to confirm that mutations have been recombined, as well as to identify the silent mutation originating from the primers, thus confirming the that the recombination event during the RCR has taken place as expected.

10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
2192
2193
2194
2195
2196
2197
2198
2199
2200
2201
2202
2203
2204
2205
2206
2207
2208
2209
2210
2211
2212
2213
2214
2215
2216
2217
2